

## Research Article

# Effects of land use on soil microbial community structure and diversity in the Yellow River floodplain

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## Abstract

Soil microorganisms and their diversity are important bioindicators of soil carbon and nutrient cycling. Land use type is a major determining factor that influences soil microbial community composition in floodplain ecosystems. However, how the structure and diversity of soil microbial communities respond to specific changes in land use, as well as the main drivers of these changes, are still unclear. This study was conducted in the Yellow River floodplain to examine the effects of land use type on soil microbial communities. Four land use types (shrubland, farmland, grassland and forest) were selected, wherein shrubland served as the baseline. We measured soil microbial structure and diversity using phospholipid fatty acids (PLFAs). Land use type significantly affected total, bacterial and fungal PLFAs, and the gram-positive/negative bacterial PLFAs. Compared with shrubland, peanut farmland had higher total and bacterial PLFAs and forest had higher fungal PLFAs. Soil pH and phosphorus were the predominate drivers of microbial PLFAs, explaining 37% and 26% of the variability, respectively. Soil total nitrogen and nitrate nitrogen were the main factors increasing microbial community diversity. Peanut farmland had the highest soil carbon content, soil carbon stock, total PLFAs and microbial diversity, suggesting that farmland has great potential as a carbon sink. Our findings indicated that peanut farmland in the Yellow River floodplain is critical for maintaining soil microbial communities and soil carbon sequestration.

**Keywords** bacteria, fungi, Yellow River floodplain, microbial community diversity, soil carbon stock, land use type

## 土地利用方式对黄河漫滩土壤微生物群落结构和多样性的影响

**摘要:** 土壤微生物群落及其多样性是土壤碳和养分循环的重要生物指标。土地利用变化是影响漫滩生态系统土壤微生物群落组成的主要决定因素。然而, 土壤微生物群落的结构和多样性如何响应土地利用变化,

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以及这些变化的主要驱动因素是什么，仍不清楚。本研究在黄河漫滩进行，以检验土地利用变化对土壤微生物群落的影响。选取了4种土地利用类型(灌丛、农田、草地和森林)，其中以灌丛地为对照，用磷脂脂肪酸测量了土壤微生物组成和多样性。研究表明，土地利用变化显著影响了总细菌、真菌和革兰氏阳性/阴性细菌。与灌丛相比，农田的总磷脂脂肪酸和细菌较高，森林的真菌较高。土壤pH值和全磷是微生物组成的最佳预测因子，分别解释了37%和26%的变异性。土壤全氮和硝态氮是影响微生物多样性的主要因素。花生农田的土壤碳含量、土壤碳储量、磷脂脂肪酸总量和微生物多样性最高，表明漫滩具有巨大的碳汇潜力。这些研究结果表明，黄河漫滩的农田对于维持土壤微生物群落和土壤碳固存至关重要。

**关键词：**细菌，真菌，黄河漫滩，微生物多样性，土壤碳储量，土地利用类型

## INTRODUCTION

Floodplains are located in ecotones at water–land interfaces, and can influence the local climate, water resource balance and biological diversity (Verones *et al.* 2013). With human population growth and increases in farming activities, nearly half of the world's floodplains have been modified (Field and Barros 2014). Different land uses in floodplain ecosystems can have numerous ecological consequences, such as shifts in the soil microbial community structure as well as carbon, nitrogen and phosphorus cycling in the soil (Guo and Zhou 2020). Soil microbes are sensitive to environmental changes, which serve as early indicators of land use type (Shao *et al.* 2019a). In addition, microbial community diversity can influence the soil carbon pools where soil biotic and abiotic properties rapidly respond to environmental shifts (Liu *et al.* 2020). Clarifying how soil microbial communities respond and adapt to different land use types will be helpful in understanding microbially driven carbon sequestration (Liu *et al.* 2018; Márton *et al.* 2017).

Microbes, which directly influence ecosystem carbon turnover and nutrient mineralization, are necessary for primary production and affect overall ecosystem sustainability (Ho *et al.* 2018; Pan *et al.* 2021; Shao *et al.* 2019b). Previous studies have demonstrated that land use significantly affects various ecosystems by changing the compositions of soil microbial communities (Ho *et al.* 2018; Lu *et al.* 2019), thereby changing the carbon cycling capacity of the soil (Chen and Sinsabaugh 2021; Ji *et al.* 2020). Evidence from the Central China Plain region has shown that the transformation of shrubland into farmland alters soil microbial community composition (bacteria and fungi) and soil carbon sequestration capacity (Zhang *et al.* 2016). Furthermore, old-growth forests converted to human-planted forests or grassland significantly

increased the abundance of gram-negative (G<sup>-</sup>) bacteria in Southwest China (Luo *et al.* 2020). Despite the research demonstrating the connection between land use and microbial communities, little is known about how land use types affect the structure and diversity of soil microbial communities in floodplains. Therefore, an accurate assessment of how land use change effects soil microbial biomass and community composition is critical to better understand soil carbon sequestration in floodplains. However, the fatty acids of soil microbial communities have not yet been fully characterized, which could lead to incomplete results and inaccurate conclusions. The phospholipid fatty acids (PLFAs) method, which covers a wide range of microbiota, has been used in similar studies to characterize the structural diversity of microbial communities (Guo *et al.* 2018; Micaela *et al.* 2021). Therefore, this study utilized the PLFA method as it is best suited for the overall analysis of microbial communities (Luo *et al.* 2020; Micaela *et al.* 2021).

The physical and chemical properties of soil are the main factors affecting microbial community structure and diversity (Liu *et al.* 2020; Yu *et al.* 2021; Zeng *et al.* 2022). When ecosystems transition from natural to disturbed, environmental conditions across all the distinct microbial habitats found in soil can be altered considerably. For example, a change in land use from natural forest to degraded forest led to a decrease in soil carbon and nitrogen, which reduced microbial activity and diversity (Kumar and Ghoshal 2017). Microbial community structure and diversity can be altered by changes in environmental variables such as phosphorus (Zhang *et al.* 2021), which is used by gram-positive (G<sup>+</sup>) bacteria to synthesize cell walls (Dong *et al.* 2014; Liu *et al.* 2020). Similarly, land use change can lead to mycelial growth and alter soil pH and bulk density (BD), which are vital soil parameters that can determine ecosystem function (Almeida *et al.* 2020; Vitali *et al.* 2016; Wang *et al.* 2018).

Floodplains are riparian areas where massive amounts of carbon and nitrogen are exchanged, and are highly sensitive to global change (Urbanová *et al.* 2015). Land use change, particularly the conversion from natural shrub covered floodplains to farmland or forest, has been a common occurrence in many areas (Sala *et al.* 2000). The Yellow River floodplain has natural and artificial land use types, making it an ideal location to investigate the effects of land use change on soil microbial community structure and diversity. In the present study, we conducted a survey covering four land use types, including shrubland, farmland, grassland and forest, in the floodplain of the Yellow River in Henan Province, China. The objectives of the study were: (i) to examine the structure and diversity of soil microbial communities in relation to land use; and (ii) to evaluate how soil physical–chemical factors drive changes in soil microbial community structure and diversity in the Yellow River floodplain.

## MATERIALS AND METHODS

### Study site

The study was conducted in a floodplain near the Yellow River, located in Henan Province, China (34°58′26″ N, 113°24′57″ E, 100 m a.s.l., Fig. 1). The area experiences a monsoon climate, with mean annual average temperature of 14 °C and mean annual precipitation of 562 mm (2000–18, local meteorological station). The soil is a sandy loam structure (76% sand, 20% silt and 4% clay in the 0–10 cm of soil layer) and was developed from alluvium parent material of the Yellow River.

In the studied area, shrubland represents the natural undisturbed ecosystem. All the land area was formed from bare riverbeds after the construction of the Xiaolangdi Dam in 2001. However, human activities had repurposed much of the land, transforming it from partial shrubland to farmland, grassland and forest around 2012. The land use history was investigated based on field interviews with the local farmers.

The dominant plant species in the natural shrubland were *Tamarix* (*Tamarix ramosissima*), *Cynodon* (*Cynodon dactylon*) and *Calamagrostis* (*Calamagrostis epigeios*). Grassland was dominated by *Cynodon* (*C. dactylon*) and *Calamagrostis* (*C. epigeios*). The primary crop planted on the farmland was peanut (*Arachis hypogaea*). The primary plant species in the artificial forest was the common Privet

(*Ligustrum vulgare*, Table 1). The floodplain in the Yellow River experiences 2–3 floods every year due to the Xiaolangdi Dam releasing water from July to October.

### Experimental design and sampling

In the studied site, the four land use types (shrubland, farmland, grassland and forest) were sampled in November 2020. In each land use type, five plots were sampled. Each plot had an area of 20 m × 20 m, with at least 200 m buffer between any two plots to avoid pseudo-replication (Li *et al.* 2020). In each plot, 0–10 cm depth soil samples were collected with a soil auger according to the cross-sampling method, including cores at each of the four corners and the middle of each plot. A total of 25 soil subsamples were obtained from each land use type, and the subsamples from each plot were pooled. Each plot served as a replicate sample, and the five replicate plot samples were kept separate. In total, there were five replicates for each of the four land use types.

To measure aboveground biomass for each land use type, we sampled 1 m × 1 m subplots. All biomass was collected at a height of 1 cm above the ground and placed in a paper bag for transportation to the laboratory. The aboveground vegetation was then dried at 105 °C in an oven, and then dried at 65 °C until constant weight to calculate aboveground biomass. The aboveground biomass of the artificial forest was evaluated using the binary power function by measuring tree diameter at breast height, tree height and crown width (Zi *et al.* 2017):

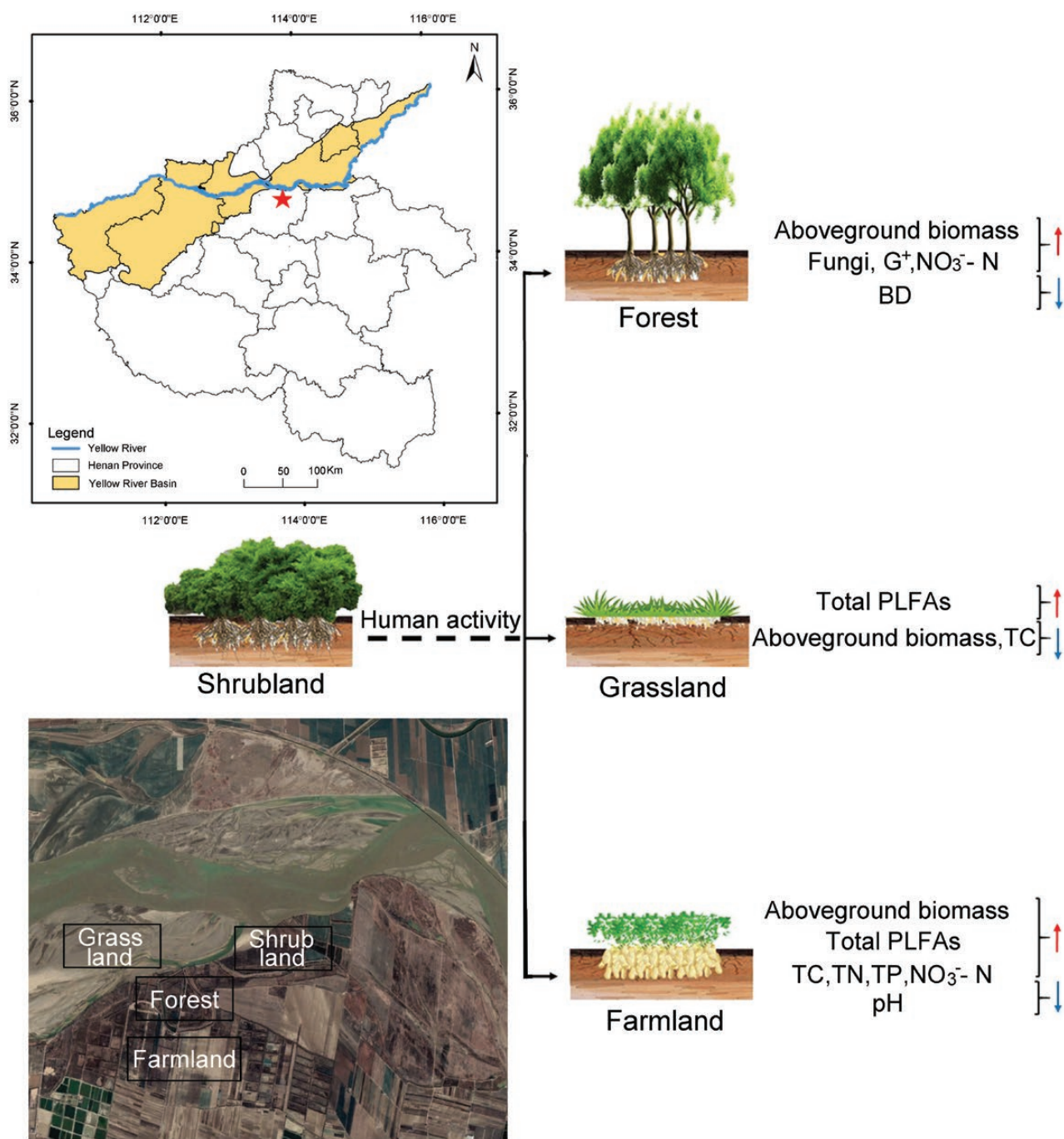
$$BM = a(DBH)^b$$

where the independent variable is DBH, which is the diameter at breast height; and *a* and *b* are coefficients.

Each sample was divided into two subsamples, which were placed in self-sealing plastic bags in an icebox and transported to the laboratory for chemical and microbial analyses. After removing all visible roots and stones, one subsample was air-dried and passed through a 0.25-mm mesh in order to measure the chemical composition of the soil, and the other subsample group was stored at –20 °C for PLFA measurements.

### Soil analysis

The soil pH was determined in a solution with a soil–water ratio of 1:2.5 using a pH meter (Sartorius PT-21, Shanghai, China). The soil BD was measured with the volumetric ring method. Soil total carbon (TC) and total nitrogen (TN) were measured using a Vario Max



**Figure 1:** Maps and schematic diagram of land use types in the Yellow River floodplain. Soil TC (g/kg), TN (g/kg), TP (g/kg),  $\text{NO}_3\text{-N}$  (mg/kg), pH, soil BD ( $\text{g/cm}^3$ ) and gram-positive ( $\text{G}^+$ ) bacterial PLFAs. The up arrows indicate significant increase and the down arrows indicate significant decreases in the listed indicators between shrubland and other land use types.

CNS elemental analyzer (Elementar Analysensysteme GmbH, Hanau, Germany). In addition, total phosphorus (TP), nitrate nitrogen ( $\text{NO}_3\text{-N}$ ) and ammonium nitrogen ( $\text{NH}_4\text{-N}$ ) were determined using an Auto Analyzer (AA3, Norderstedt, Germany). The total soil carbon stock (SCS) was calculated according to the following equation (Luo *et al.* 2020):

$$\text{SCS} = \sum_{i=1}^n (C_i \times \text{BD} \times h_i) / 10$$

where  $n$  is the number of soil layers,  $C_i$  is the soil total carbon content (g/kg) of the  $i$ th layer and  $h_i$  is the thickness of soil (cm).

**Table 1:** Dominant plant species and aboveground biomass in shrubland, farmland, forest and grassland

	Dominant plant species	Aboveground biomass (g/m <sup>2</sup> )
Shrubland	<i>Tamarix ramosissima</i> , <i>Cynodon dactylon</i> , <i>Calamagrostis epigejos</i>	468.9 ± 56.02 C
Farmland	<i>Arachis hypogaea</i>	889.6 ± 15.41 B
Forest	<i>Ligustrum vulgare</i>	5197.7 ± 47.16 A
Grassland	<i>Cynodon dactylon</i> , <i>Calamagrostis epigeios</i>	350.2 ± 44.31 D

Values are the means ± standard error ( $n = 5$ ). Different capital letters indicate significant differences ( $P < 0.05$ ) among the different land use types.

### Analysis of PLFAs

The soil microbial PLFAs were determined by gas chromatography (Agilent Technologies 7890A, Zhao *et al.* 2016). PLFAs were extracted from fresh soil (8 g dry weight equivalent) with a single-phase mixture (1:2:0.8, v/v/v) containing chloroform, methanol and phosphate buffer. Using 19:0 methyl esters as the internal standard. The fatty acid fractions of PLFAs were analyzed separately on a gas chromatograph with a flame ionization detector (FID) (GC6890, Agilent Technologies, Bracknell, UK) by automatic injection of samples. Characteristic fatty acids were grouped into biomarkers, as shown in Supplementary Table S1.

Microbial community diversity was calculated using the Shannon–Weiner diversity index ( $H$ ), the Pielou evenness index ( $J$ ) and the Margalef richness index ( $R$ ) (Wang *et al.* 2012; Zak *et al.* 1994).

$$H = - \sum_{i=1}^s P_i \ln P_i$$

where  $s$  is the number of characteristic fatty acids and  $P_i$  is the measure of  $i$ th species proportional to the total number of species.

$$J = H / \ln S$$

$$R = (S - 1) / \ln N$$

where  $N$  is the total number of individuals and  $S$  is the total number of species in each sample.

### Statistical analyses

The soil variable and soil microbial PLFAs were examined for normality and transformed using log<sub>10</sub> to satisfy the assumptions of the statistical analyses. The effects of land use type on soil variables (BD, TC, TN, TP, C/N ratio, pH, NH<sub>4</sub>-N and NO<sub>3</sub>-N) and soil microbial PLFAs (total PLFAs, bacterial and fungal PLFAs, bacteria/fungi ratio, gram-positive and -negative bacterial PLFAs, gram-positive/negative

bacteria ratio, Actinomycetes, Shannon–Weiner index, Pielou index and Margalef index) were examined by one-way analysis of variance (ANOVA). The least significant difference (LSD) multiple comparisons ( $P < 0.05$ ) was used to identify significant effects. The Spearman's correlation coefficient and redundancy analysis were performed to quantify the correlations between the soil microbial structure and diversity and soil variables in the R software environment (version 3.2.2, R Core Team 2015).

## RESULTS

### Soil physical–chemical characteristics

Land use significantly affected the soil TC, TN, TP, NO<sub>3</sub>-N, pH, soil BD and soil carbon density ( $P < 0.05$ , Table 2). Compared with shrubland, soil TC content was significantly lower in grassland and significantly higher in farmland ( $P < 0.05$ ). The SCS in farmland was significantly higher than shrubland, the mean values increased 29% ( $P < 0.01$ ). The TN and TP contents in farmland were significantly higher than those in shrubland and grassland soils ( $P < 0.05$ ). Land use change also significantly affected soil NO<sub>3</sub>-N content; increases of 712% were observed in farmland compared with shrubland, and values increases 211% for artificial forest compared with shrubland (both  $P < 0.01$ ). There was no significant difference in NO<sub>3</sub>-N content between shrubland and grassland soils ( $P > 0.05$ ). Additionally, the mean soil pH values of farmland and forest plots were 8.11 and 8.22, which was lower than that in the shrubland (both  $P < 0.05$ , Table 2).

### PLFAs and diversity of soil microbes

Compared with shrubland, farmland had a higher total PLFA content ( $P < 0.05$ , Fig. 2a). Furthermore, the amounts of bacterial PLFAs in farmland and grassland soils were 7% and 5% higher than in forest soil (both  $P < 0.05$ ). The highest amounts of

**Table 2:** Soil TC (g/kg), TN (g/kg), TP (g/kg), the ratio of TC to TN (C/N),  $\text{NH}_4\text{-N}$  (mg/kg),  $\text{NO}_3\text{-N}$  (mg/kg), pH, soil BD ( $\text{g/cm}^3$ ) and SCS ( $\text{kg/m}^2$ ) in shrubland, farmland, forest and grassland

	TC	TN	TP	C/N	$\text{NH}_4\text{-N}$	$\text{NO}_3\text{-N}$	pH	BD	SCS
Shrubland	23.71 ± 0.51 B	0.64 ± 0.17 B	0.90 ± 0.07 B	39.52 ± 15.69 A	0.11 ± 0.06 A	0.70 ± 0.07 C	8.33 ± 0.03 A	1.11 ± 0.03 A	26.43 ± 0.45 B
Farmland	27.02 ± 0.80 A	1.04 ± 0.03 A	1.07 ± 0.11 A	25.98 ± 1.03 A	0.15 ± 0.03 A	5.69 ± 0.91 A	8.11 ± 0.02 C	1.26 ± 0.10 A	34.11 ± 1.31 A
Forest	23.08 ± 1.55 B	0.93 ± 0.08 AB	0.89 ± 0.12 B	24.91 ± 0.74 A	0.20 ± 0.33 A	2.18 ± 0.86 B	8.22 ± 0.04 B	1.03 ± 0.08 B	17.34 ± 0.99 C
Grassland	17.16 ± 3.14 C	0.67 ± 0.16 B	0.89 ± 0.03 B	27.72 ± 2.99 A	0.09 ± 0.11 A	0.41 ± 0.23 C	8.33 ± 0.02 A	0.98 ± 0.14 B	23.67 ± 1.23 B
F value	16.47***	3.92*	3.6*	NS	NS	42.08***	10.12**	5.05**	41.96***

All data are presented as mean ± standard error ( $n = 5$ ). Different capital letters indicate significant differences ( $P < 0.05$ ) among the four land use types according to one-way ANOVA. \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ .

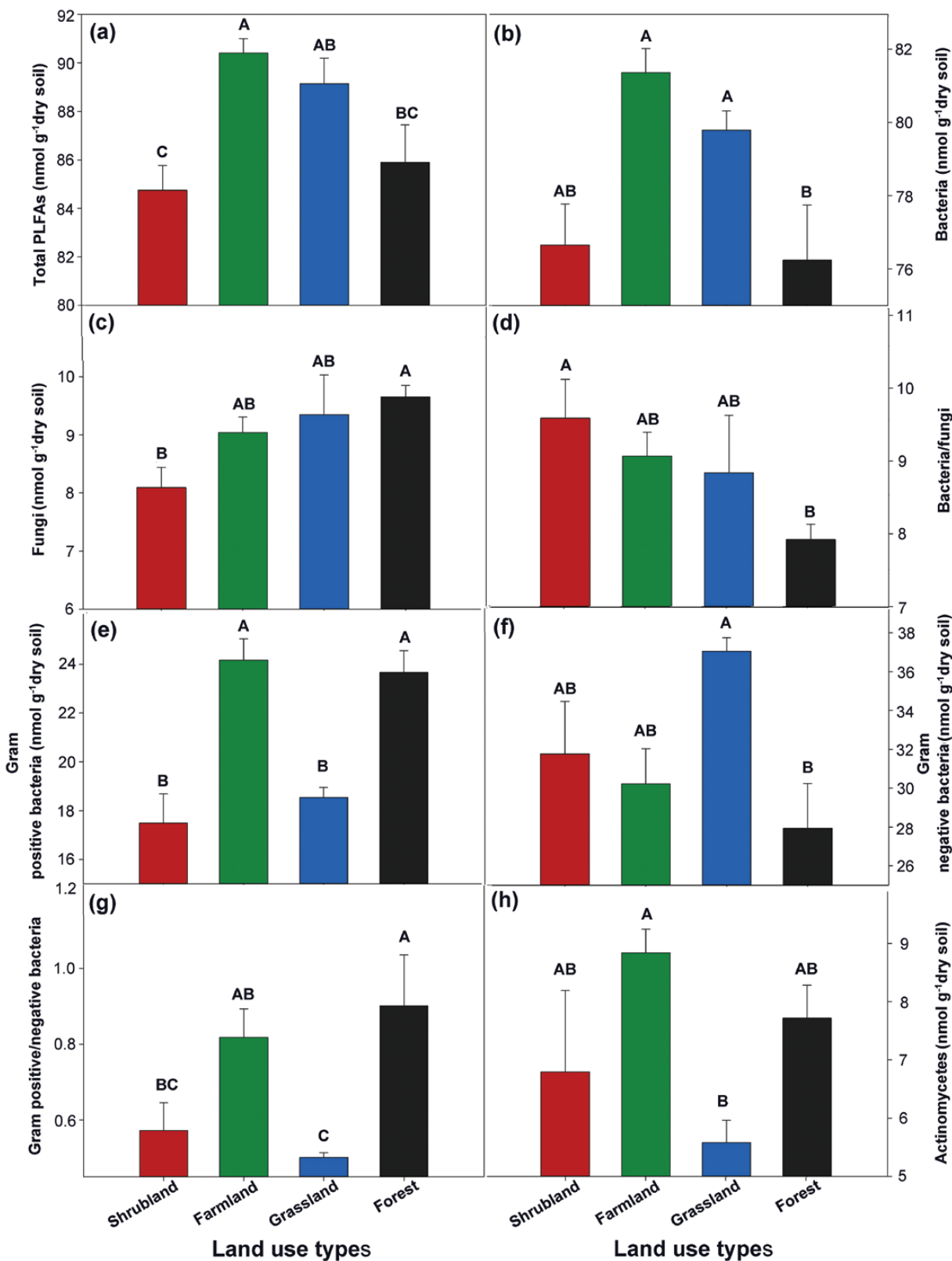
fungal PLFAs were observed in forest soil, which was significantly higher than that of shrubland soil (Fig. 2c) by an average of 19% ( $P < 0.05$ ). The highest soil bacteria/fungi ratio was observed in shrubland, which was significantly higher than that of forest (Fig. 2d).

The amounts of  $G^+$  bacteria PLFAs in the farmland and forest were significantly higher than that of shrubland by averages of 38% and 35%, respectively ( $P < 0.05$ , Fig. 2e). The  $G^+/G^-$  bacterial ratio observed in the forest soil was significantly higher than in the shrubland and grassland (Fig. 2g). The amount of Actinomycete PLFAs in the farmland was significantly higher than in the grassland (Fig. 2h). Farmland and artificial forest exhibited high Shannon–Weiner diversity index and Pielou evenness index values, which were significantly higher than for shrubland, but no differences among four land use types were observed in the Margalef index (Fig. 3a–c).

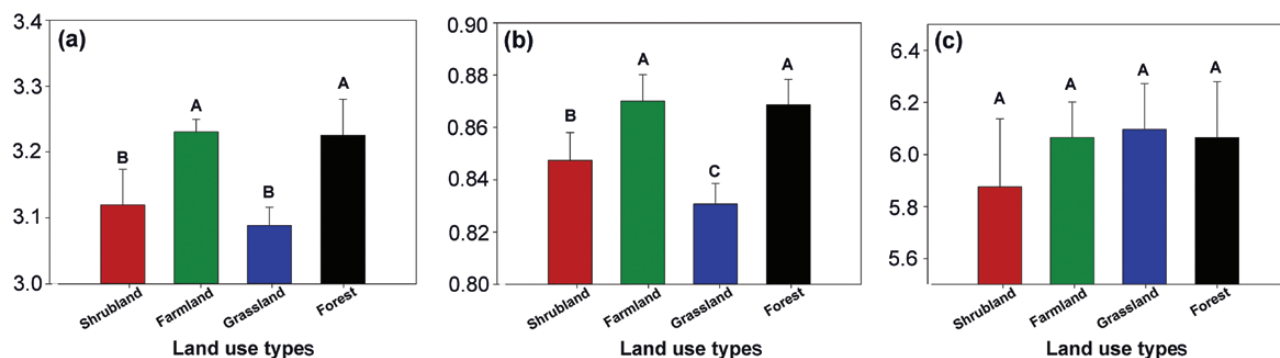
### Correlations between microorganisms and environmental factors

The Spearman's correlation analysis showed that the Actinomycetes PLFAs, Shannon–Weiner index and Pielou index were significantly positively correlated with soil TC content ( $P < 0.05$ , Table 3). The bacteria, gram-positive bacteria, Shannon–Weiner index and Pielou index were significantly positively correlated with soil TN content ( $P < 0.05$ ). The total amount of PLFAs, gram-positive bacteria and Pielou index were positively correlated with soil TP content ( $P < 0.05$ ). The Actinomycetes PLFA, gram-positive bacteria, Shannon–Weiner index and Pielou index had significant positive correlations with  $\text{NO}_3\text{-N}$  content ( $P < 0.05$ ). The fungal PLFAs were significantly positively correlated with soil BD ( $P < 0.05$ ). Gram-positive bacteria, gram-positive/negative ratio and Shannon–Weiner diversity index were negatively correlated with soil pH ( $P < 0.05$ ).

Redundancy analysis between the compositions of soil microbial communities and soil physical–chemical properties showed that the first axis explained 26% of the total variance in the soil microbial communities, and the second axis explained 24% of the total variance (Fig. 4). The forward selection of the variables in the redundancy analysis showed that soil microbial community composition across these four land use types were primarily affected by pH and TP, which explained 37% and 26% of the variability, respectively.



**Figure 2:** Soil total PLFAs (a), bacterial PLFAs (b), fungal PLFAs (c), bacteria/fungi ratio (d), gram-positive bacterial PLFAs (e), gram-negative bacterial PLFAs (f), gram-positive/negative ratio (g) and Actinomycetes PLFAs (h) in shrubland, farmland, grassland and forest. Values are the means  $\pm$  standard errors ( $n = 5$ ). Significant difference among the four land use types is denoted with different capital letters ( $P < 0.05$ ).



**Figure 3:** Shannon–Weiner (a), Pielou (b) and Margalef (c) indexes of soil microbial PLFAs in shrubland, farmland, grassland and forest. Different capital letters indicate significant differences among the four land use types ( $P < 0.05$ ).

**Table 3:** Spearman's correlation coefficients among microbial PLFAs and environmental variables across the four land use types

	Total PLFA	Gram-negative bacteria	Gram-negative bacteria	Actinomycetes	Bacteria	Fungi	Shannon–Weiner	Margalef	
TC	0.06	<b>−0.48*</b>	0.43	<b>0.55*</b>	0.11	−0.14	<b>0.71**</b>	<b>0.72**</b>	0.02
TN	0.02	−0.28	<b>0.57*</b>	0.29	0.17	−0.10	<b>0.49*</b>	<b>0.63**</b>	0.16
TP	<b>0.58*</b>	−0.10	<b>0.48*</b>	0.36	<b>0.69**</b>	0.18	0.36	0.39	0.19
NH <sub>4</sub> <sup>+</sup>	0.33	−0.22	0.23	0.43	<b>0.51*</b>	−0.07	0.03	0.04	−0.02
NO <sub>3</sub> <sup>−</sup>	0.21	−0.40	<b>0.55*</b>	<b>0.52*</b>	0.15	0.16	<b>0.67**</b>	<b>0.69**</b>	0.05
pH	−0.27	0.32	<b>−0.72**</b>	−0.19	−0.18	−0.31	<b>−0.58*</b>	<b>−0.61**</b>	−0.11
C/N	0.07	0.34	<b>−0.55*</b>	−0.19	0.06	−0.03	<b>−0.51*</b>	<b>−0.58**</b>	−0.03
BD	−0.01	−0.37	0.31	0.38	0.21	<b>−0.55*</b>	0.34	0.34	−0.22

Note: Soil TC (g/kg), TN (g/kg), TP (g/kg), NH<sub>4</sub><sup>+</sup> (mg/kg), NO<sub>3</sub><sup>−</sup> (mg/kg), pH, the ratio of TC to TN (C/N) and soil BD (g/cm<sup>3</sup>). Bold values indicate significant effects. \* $P < 0.05$ , \*\* $P < 0.01$ .

## DISCUSSION

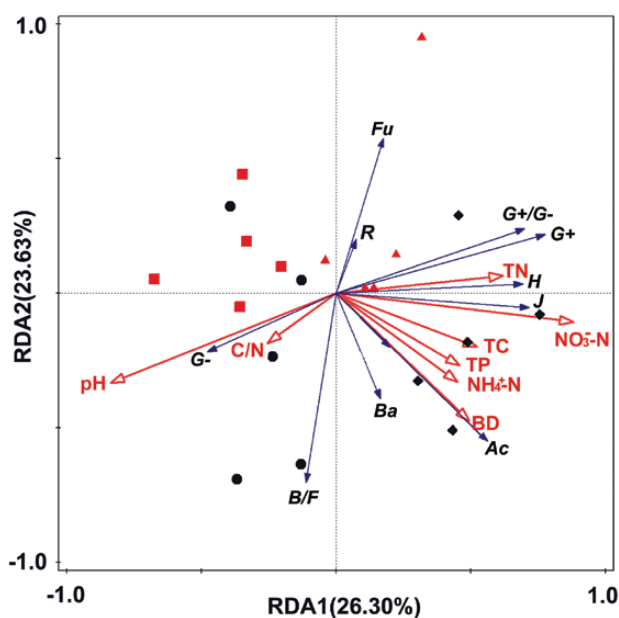
### Soil microbial PLFAs under different land uses

Soil microbial community structure and diversity differed between land use types, indicating that active microbial communities are sensitive to different land uses in the Yellow River floodplain. The differences in soil physical–chemical characteristics may be attributed to different types of vegetation and field management practices (degrees of soil disturbance and nutrient additions), which can alter soil microbial communities and soil nutrient dynamics.

Previous studies have observed decreases in the PLFAs of bacterial, gram-positive bacteria and fungi when natural vegetation transitions into farmland, reducing carbon sequestration capacity (Deng *et al.* 2015;

Katulanda *et al.* 2018; Zhang *et al.* 2016). We observed that total PLFAs, and bacterial and gram-positive PLFAs, were higher in farmland than in shrubland, which was inconsistent with previous studies (Schroeder *et al.* 2020; Wei *et al.* 2020). One explanation could be that fertilizer in farmland led to the increase in microbial biomass (Ma *et al.* 2022), which fixed more carbon in soils and increased microbial necromass that accounted for a large proportion of the soil carbon pool (Bwa *et al.* 2021; Ma *et al.* 2022). A meta-analysis showed that fertilizer has a positive effect on the total PLFA and microbial biomass, which are related to the soil nitrogen and phosphorus increases in the farmland (Alicia *et al.* 2022). In addition, peanuts are legumes and were cultivated as the main crop in the farmland of our study area; they are known to increase soil organic carbon sequestration potential compared





**Figure 4:** Redundancy analysis (RDA) of associations among soil microbial community components (as indicated by PLFAs) with environmental factors. Total PLFAs, bacterial PLFAs (Ba), fungal PLFAs (Fu), ratio of bacteria to fungi (B/F), gram-positive bacteria ( $G^+$ ), gram-negative ( $G^-$ ) bacteria, ratio of gram-positive to -negative bacteria ( $G^+/G^-$ ), Actinomycetes (Ac); three microbial indexes (Shannon–Weiner diversity index, Pielou evenness index and Margalef richness index), and eight environmental variables: soil TC, TN, TP,  $\text{NO}_3\text{-N}$ ,  $\text{NH}_4\text{-N}$ , ratio of TC to TN (C/N), pH and soil BD. Circles: grassland; diamonds: farmland; squares: shrubland; triangles: forest.

with other cropping systems (Ahmad *et al.* 2022). Moreover, the carbon and nitrogen content of the Yellow River floodplain was lower than in comparable studies (Barreiro *et al.* 2015; Schroeder *et al.* 2020; Tian *et al.* 2010; Wei *et al.* 2020; Yang *et al.* 2020), but these values are context-dependent and initial conditions can have a large influence. Therefore, both fertilizer and crop choice (peanuts) may be the main reasons for the differences observed in the Yellow River floodplain farmland compared with other farmlands.

Another reason for the observed differences between the land use types may have been the soil pH, which has previously been identified as the best predictor of microbial community composition (Qin *et al.* 2017; Wang *et al.* 2020). The difference in soil pH can be due to fertilizer input, which can interfere with a microorganism's habitat in farmland. Indeed, the addition of chemical fertilizer during farming can acidify the soil (Hao *et al.* 2022; Kimmel *et al.* 2020). The pH of bacterial cytoplasm is close to neutral, and if it shifts toward being more alkaline or acidic, there can be a negative effect on intracellular PLFA

(Eldor 2007). In this study, the soil was alkaline, so the decrease in pH brought it closer to neutral, which may have been conducive to microbial growth (Wang *et al.* 2020).

Fungal PLFAs were higher in the forest than in the shrubland, which is consistent with previous studies (Guo *et al.* 2018). This is likely a consequence of higher nutrient transformation rates and better litter quality and quantity (Collado *et al.* 2021). In our study, the forest had the highest aboveground biomass (Table 1), which should translate into much more litter that can have a positive effect on microbial growth, especially fungi (Urbanová *et al.* 2015). The increased fungal PLFAs in the forest compared with the shrubland could have potentially resulted from fungi infecting the roots of the young privet trees (Grayston *et al.* 2004; Wakelin *et al.* 2008). Arbuscular mycorrhizal fungi enhance nutrient availability to plants, particularly phosphorus, due to their extensive mycorrhizal mycelium networks that increase the surface area available for phosphorus acquisition (Eldor 2007). This may be one of the reasons why forest and grassland soils had the lowest phosphorus contents, but relatively high fungal biomass. Compared with shrubland, the higher fungal biomass in forest soil was related to the lower soil BD. This result was consistent with the observations of Wang *et al.* (2017), who found that soil disturbance had an important effect on fungal biomass. The high total PLFAs and bacterial and gram-positive bacterial biomass in farmland can be an effect of the high soil nitrogen and phosphorus supplied by fertilization. Overall, fertilizer may have enhanced the bacterial abundance in the farmland, especially in nitrogen-poor areas such as the Yellow River floodplain (Chen *et al.* 2022; Tian *et al.* 2010).

### Microbial diversity under different land uses

Microbial diversity has been shown to contribute to carbon use efficiency (Chen *et al.* 2015; Domeignoz-Horta *et al.* 2020; Wu *et al.* 2022). Differences in soil microbial community diversity due to land use changes may influence the stability of the soil carbon pool (Wang *et al.* 2018; Zheng *et al.* 2020). The changes in physical–chemical properties are strongly related to changes in microbial PLFAs and diversity of floodplain soils (Dhandapani *et al.* 2020). Increasing soil TN, TP and  $\text{NO}_3\text{-N}$  supply, which are sources of nutrients and energy, can stimulate microbial activity (Zhou *et al.* 2019) by providing more sustenance for underground microbial communities (Chu *et al.* 2010; Djighaly *et al.* 2020; Zhang *et al.* 2022).

The high Shannon–Weiner diversity index values for farmland and forest were consistent with previous studies (Cui *et al.* 2021; Yang *et al.* 2020), i.e. the microbial diversities in the modified ecosystems, i.e. farmland, artificial forest and grassland, were significantly higher than the natural ecosystems, i.e. shrubland. In our study, the soil TC and TN were significantly correlated with Shannon–Weiner diversity index. The application of fertilizer in the modified ecosystems can potentially increase microbial diversity. Microbes mainly prevent release of carbon by stabilizing it into a form i.e. not easily decomposed (Liang *et al.* 2017). Therefore, higher microbial diversity plays an important role in carbon sequestration in artificial ecosystems.

Our results were inconsistent with some previous studies that have observed the destruction of soil by mechanized planting and changes in soil pH caused by fertilizer to destroy the microorganism habitat in farmland (Guo *et al.* 2018; Leeuwen *et al.* 2017; Qin *et al.* 2017). This may have been because the cultivation of peanuts in farmland led to increased fixation of rhizobia, which will fix nitrogen from the atmosphere to the soil, resulting in an abundant supply of nutrients for microbes, thereby increasing diversity (Xie *et al.* 2019). It may also have been because the selection of specific microorganisms by different plant communities, such as legumes, facilitates certain types of bacteria and leads to increased microbial diversity in farmland (Huang *et al.* 2020). Indeed, the different crops grown on farmland can produce differences in microbial diversity. A meta-analysis showed that cultivating legumes has a higher carbon sequestration potential than other crops, such as wheat and cotton (Jian *et al.* 2020). These results indicated that there is likely to be significant variability in structural and functional responses of microbial communities to land use change, with potential consequences in terms of soil carbon cycling.

Despite the clear evidence provided here that land use type significantly affects soil microbial community composition, there are several uncertainties and limitations that should be mentioned. First, the fact that the species composition of each land use type was relatively simple dampens the potential of carbon sequestration in Yellow River floodplain. Second, we only investigated the response of microorganisms to shifts in land use over a short-term period (from 2012 to 2020), but the microbial response to land use was time dependent. Therefore, to better clarify the impact of different land use types on soil carbon

and to provide reliable evidence, long-term and continuous monitoring of multiple land use types should be carried out.

## CONCLUSIONS

Land use significantly influenced the total PLFAs, bacterial PLFAs and Shannon–Weiner diversity index, which were highest in peanut farmland. The peanut farmland had the largest total soil carbon content and SCS (0–10 cm). Soil TN, TP and NO<sub>3</sub>-N were positive indicators of microbial biomass and diversity, and pH was a negative indicator. These findings suggested that altering the land use type changed the physicochemical characteristics of the soils, which affected the composition of microbial communities.

### Supplementary Material

Supplementary material is available at *Journal of Plant Ecology* online.

Table S1: Biomarkers for microbial grope.

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